



CORRECTED SEQUENCE LISTING

RECEIVED

MAY 22 2003

TECH CENTER 1600/2900

<110> Conseiller, Emmanuel  
Debussche, Laurent  
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 33

B- <170> PatentIn version 3.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-1(p53)

<400> 1

agatctgtat ggaggagccg cag

23

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<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' -393 (p53)

<400> 2  
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29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide H175 3'

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ggggcagtgc ctcac

15

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<211> 15

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<223> oligonucleotide w248 3'

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gggcctccag ttcac

15

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<211> 15

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide H273 3'

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acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

<213> Artificial Sequence

B'-contd

<220>  
 <223> oligonucleotide G281 3'

<400> 6  
 gcgccggcct ctccc 15

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<211> 23

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<213> Artificial Sequence

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 <223> oligonucleotide 5'-73

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<210> 8

<211> 1021

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<213> Artificial Sequence

<220>  
 <223> Murine MBP1 C-term fragment

<220>  
 <221> CDS  
 <222> (1)..(885)

<400> 8  
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 Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
 1 5 10 15

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg 96  
 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct 144  
 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca 192  
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt 240  
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80

aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc 288

B'-contd

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95  
 gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac 336  
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110  
 gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg 384  
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125  
 gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac 432  
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
 130 135 140  
 caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc 480  
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160  
 tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac 528  
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
 165 170 175  
 aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct 576  
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
 180 185 190  
 tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg 624  
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
 195 200 205  
 cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc 672  
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
 210 215 220  
 tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac 720  
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240  
 att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca 768  
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255  
 gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg 816  
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270  
 aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc 864  
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285  
 ttt gtg gga gcc tat acc ttc tgaagaccct caggggaagg ccatgtgggg 915  
 Phe Val Gly Ala Tyr Thr Phe  
 290 295  
 gcccttccc cctcccatag cttaagcagc cccgggggcc tagggatgac cgttctgctt 975  
 aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa 1021

<210> 9

<211> 295

<212> PRT

<213> Artificial sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

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1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala

210

215

220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

Phe Val Gly Ala Tyr Thr Phe  
 290 295

&lt;210&gt; 10

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide c-myc 5'

&lt;400&gt; 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

&lt;210&gt; 11

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide c-myc 3'

&lt;400&gt; 11

gatctcaggt cctcctcgga gatcagcttc tgctccatg

39

&lt;210&gt; 12

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> 5' MCS oligonucleotide

<400> 12  
gatctcgggtc gacctgcatg caattcccgg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>  
<223> 3' MCS oligonucleotide

<400> 13  
cgcgggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>  
<223> Oligonucleotide 3' mMBP1

<400> 14  
cgttactggc agaggtaact gg

22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>  
<223> MBP1 murine (complete sequence)

<220>  
<221> CDS  
<222> (49)..(1377)

<400> 15  
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Met Leu Pro  
1

57

ttt Phe 5	gcc Ala	tcc Ser	tgc Cys	ctc Leu	ccc Pro	ggg Gly 10	tct Ser	ttg Leu	ctg Leu	ctc Leu	tgg Trp 15	gcg Ala	ttt Phe	ctg Leu	ctg Leu	105
ttg Leu 20	ctc Leu	ttg Leu	gga Gly	gca Ala	gcg Ala 25	tcc Ser	cca Pro	cag Gln	gat Asp	ccc Pro 30	gag Glu	gag Glu	ccg Pro	gac Asp	agc Ser 35	153
tac Tyr	acg Thr	gaa Glu	tgc Cys	aca Thr 40	gat Asp	ggc Gly	tat Tyr	gag Glu	tgg Trp 45	gat Asp	gca Ala	gac Asp	agc Ser	cag Gln 50	cac His	201
tgc Cys	cgg Arg	gat Asp	gtc Val 55	aac Asn	gag Glu	tgc Cys	ctg Leu	acc Thr 60	atc Ile	ccg Pro	gag Glu	gct Ala	tgc Cys 65	aag Lys	ggc Gly	249
gag Glu	atg Met	aaa Lys 70	tgc Cys	atc Ile	aac Asn	cac His	tac Tyr 75	ggg Gly	ggc Gly	tat Tyr	ttg Leu	tgt Cys 80	ctg Leu	cct Pro	cgc Arg	297
tct Ser	gct Ala 85	gcc Ala	gtc Val	atc Ile	agt Ser	gat Asp 90	ctc Leu	cat His	ggc Gly	gaa Glu	gga Gly 95	cct Pro	cca Pro	ccg Pro	cca Pro	345
gcg Ala 100	gcc Ala	cat His	gct Ala	caa Gln	caa Gln 105	cca Pro	aac Asn	cct Pro	tgc Cys	ccg Pro 110	cag Gln	ggc Gly	tac Tyr	gag Glu	cct Pro 115	393
gat Asp	gaa Glu	cag Gln	gag Glu	agc Ser 120	tgt Cys	gtg Val	gat Asp	gtg Val	gac Asp 125	gag Glu	tgt Cys	acc Thr	cag Gln	gct Ala 130	ttg Leu	441
cat His	gac Asp	tgt Cys	cgc Arg 135	cct Pro	agt Ser	cag Gln	gac Asp	tgc Cys 140	cat His	aac Asn	ctt Leu	cct Pro	ggc Gly 145	tcc Ser	tac Tyr	489
cag Gln	tgc Cys	acc Thr 150	tgc Cys	cct Pro	gat Asp	ggc Gly	tac Tyr 155	cga Arg	aaa Lys	att Ile	gga Gly	ccc Pro 160	gaa Glu	tgt Cys	gtg Val	537
gac Asp	ata Ile 165	gat Asp	gag Glu	tgt Cys	cgt Arg	tac Tyr 170	cgc Arg	tat Tyr	tgc Cys	cag Gln	cat His 175	cga Arg	tgt Cys	gtg Val	aac Asn	585
ctg Leu 180	ccg Pro	ggc Gly	tct Ser	ttt Phe	cga Arg 185	tgc Cys	cag Gln	tgt Cys	gag Glu	cca Pro 190	ggc Gly	ttc Phe	cag Gln	ttg Leu	gga Gly 195	633
cct Pro	aac Asn	aac Asn	cgc Arg	tct Ser 200	tgt Cys	gtg Val	gat Asp	gtg Val	aat Asn 205	gag Glu	tgt Cys	gac Asp	atg Met	gga Gly 210	gcc Ala	681
cca Pro	tgt Cys	gag Glu	cag Gln 215	cgc Arg	tgc Cys	ttc Phe	aac Asn	tcc Ser 220	tat Tyr	ggg Gly	acc Thr	ttc Phe	ctg Leu 225	tgt Cys	cgc Arg	729
tgt Cys	aac Asn	cag Gln 230	ggc Gly	tat Tyr	gag Glu	ctg Leu	cac His 235	cgg Arg	gat Asp	ggc Gly	ttc Phe	tcc Ser 240	tgc Cys	agc Ser	gat Asp	777
atc Ile	gat Asp 245	gag Glu	tgc Cys	ggc Gly	tac Tyr	tcc Ser 250	agt Ser	tac Tyr	ctc Leu	tgc Cys	cag Gln 255	tac Tyr	cgc Arg	tgt Cys	gtc Val	825



aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu 260 265 270 275	873
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala 280 285 290	921
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr 295 300 305	969
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser 310 315 320	1017
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln 325 330 335	1065
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser 340 345 350 355	1113
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly 360 365 370	1161
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe 375 380 385	1209
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg 390 395 400	1257
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr 405 410 415	1305
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr 420 425 430 435	1353
gtc ttt gtg gga gcc tat acc ttc tgaagaccct caggggaagg ccattgtggg Val Phe Val Gly Ala Tyr Thr Phe 440	1407
gcccccttccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa	1513

<210> 16

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
 260 265 270  
 Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
 275 280 285  
 Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
 290 295 300  
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
 305 310 315 320  
 Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
 325 330 335  
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
 340 345 350  
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
 355 360 365  
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
 370 375 380  
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
 385 390 395 400  
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
 405 410 415  
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430  
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
 435 440

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' hMBP1

<400> 17  
ctccgctccg aggtgatggt c 21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5' hMBP1

<400> 18  
tgtagctact ccagctacct c 21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 19  
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gctcccctgc gcctcctgcc taccggggtc tctactgctc tgggcgctgc tactgttgct 120  
cttgggatca gcttctctc aggattctga agagcccgac agctacacgg aatgcacaga 180  
tggctatgag tgggaccag acagccagca ctgccgggat gtcaacgagt gtctgaccat 240  
ccctgaggcc tgcaaggggg aaatgaagt catcaaccac tacgggggct acttgtgcct 300  
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tcccgctcaa caccccaacc cctgcccacc aggctatgag cccgacgatc aggacagctg 420  
tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cggcccagcc aggactgcca 480  
taacttgctt ggctcctatc agtgcacctg ccctgatggt taccgcaaga tcggggcccga 540  
gtgtgtggac atagacgagt gccgctaccg ctactgccag caccgctgcg tgaacctgcc 600  
tggctccttc cgctgccagt gcgagccggg cttccagctg gggcctaaca accgctcctg 660  
tgttgatgtg aacgagtgtg acatgggggc cccatgagag cagcgtgct tcaactccta 720  
tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg 780  
cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga 840  
gccaggccgt ttctcctgcc actgcccaca gggttaccag ctgctggcca cagcctctg 900

ccaagacatt gatgagtgtg agtctggtgc gcaccagtgc tccgaggccc aaacctgtgt 960  
 caacttccat gggggctacc gctgctgga caccaaccgc tgcgtggagc cctacatcca 1020  
 ggtctctgag aaccgctgtc tctgcccggc ctccaaccct ctatgtcgag agcagccttc 1080  
 atccattgtg caccgctaca tgaccatcac ctcggagcgg ag 1122

<210> 20

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 20

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 tgccactgcc cacagggtta ccagctgctg gccacacgcc tctgccaaga cattgatgag 120  
 tgtgagtctg gtgctcacca gtgctccgag gcccaaacct gtgtcaactt ccatgggggc 180  
 taccgctgctg tggacaccaa ccgctgctg gagccctaca tccaggtctc tgagaaccgc 240  
 tgtctctgcc cggcctccaa ccctctatgt cgagagcagc cttcatccat tgtgcaccgc 300  
 tacatgacca tcacctcgga gcggagcgtg cccgctgacg tgttccagat ccaggcgacc 360  
 tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaactc gcagggggac 420  
 ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctcgcccc gccggtgacg 480  
 ggcccccggg agtacgtgct ggacctggag atggtcacca tgaattccct catgagctac 540  
 cgggccagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca 600  
 ggagggagacc accctccctg cagctaccct agctgaggag cctgtttgtga ggggcagaat 660  
 gagaaaggca ataaaggag aaag 684

<210> 21

<211> 1480

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

aagccagccg agccgccaga gccgcgggcc gcgggggtgt cgcgggccca accccagg 58

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Met	Leu	Pro	Cys	Ala	Ser	Cys	Leu	Pro	Gly	Ser	Leu	Leu	Leu	Trp	Ala	
1				5					10					15		
ctg	cta	ctg	ttg	ctc	ttg	gga	tca	gct	tct	cct	cag	gat	tct	gaa	gag	154
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Ala	Ser	Pro	Gln	Asp	Ser	Glu	Glu	
			20					25					30			
ccc	gac	agc	tac	acg	gaa	tgc	aca	gat	ggc	tat	gag	tgg	gac	cca	gac	202
Pro	Asp	Ser	Tyr	Thr	Glu	Cys	Thr	Asp	Gly	Tyr	Glu	Trp	Asp	Pro	Asp	
		35					40					45				
agc	cag	cac	tgc	cgg	gat	gtc	aac	gag	tgt	ctg	acc	atc	cct	gag	gcc	250
Ser	Gln	His	Cys	Arg	Asp	Val	Asn	Glu	Cys	Leu	Thr	Ile	Pro	Glu	Ala	
	50					55					60					
tgc	aag	ggg	gaa	atg	aag	tgc	atc	aac	cac	tac	ggg	ggc	tac	ttg	tgc	298
Cys	Lys	Gly	Glu	Met	Lys	Cys	Ile	Asn	His	Tyr	Gly	Gly	Tyr	Leu	Cys	
65					70					75					80	
ctg	ccc	cgc	tcc	gct	gcc	gtc	atc	aac	gac	cta	cac	ggc	gag	gga	ccc	346
Leu	Pro	Arg	Ser	Ala	Ala	Val	Ile	Asn	Asp	Leu	His	Gly	Glu	Gly	Pro	
				85					90					95		
ccg	cca	cca	gtg	cct	ccc	gct	caa	cac	ccc	aac	ccc	tgc	cca	cca	ggc	394
Pro	Pro	Pro	Val	Pro	Pro	Ala	Gln	His	Pro	Asn	Pro	Cys	Pro	Pro	Gly	
			100					105					110			
tat	gag	ccc	gac	gat	cag	gac	agc	tgt	gtg	gat	gtg	gac	gag	tgt	gcc	442
Tyr	Glu	Pro	Asp	Asp	Gln	Asp	Ser	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	
		115					120					125				
cag	gcc	ctg	cac	gac	tgt	cgc	ccc	agc	cag	gac	tgc	cat	aac	ttg	cct	490
Gln	Ala	Leu	His	Asp	Cys	Arg	Pro	Ser	Gln	Asp	Cys	His	Asn	Leu	Pro	
	130					135					140					
ggc	tcc	tat	cag	tgc	acc	tgc	cct	gat	ggt	tac	cgc	aag	atc	ggg	ccc	538
Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro	
145					150				155						160	
gag	tgt	gtg	gac	ata	gac	gag	tgc	cgc	tac	cgc	tac	tgc	cag	cac	cgc	586
Glu	Cys	Val	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg	
				165					170					175		
tgc	gtg	aac	ctg	cct	ggc	tcc	ttc	cgc	tgc	cag	tgc	gag	ccg	ggc	ttc	634
Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe	
			180					185					190			
cag	ctg	ggg	cct	aac	aac	cgc	tcc	tgt	gtt	gat	gtg	aac	gag	tgt	gac	682
Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp	
		195					200					205				
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	ttc	aac	tcc	tat	ggg	acc	ttc	730
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	
	210					215					220					
ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	778
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	
					230					235					240	
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	826
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	
				245					250					255		

cg	tc	gt	aa	ga	cc	gg	cg	tt	tc	tg	ca	tg	cc	ca	gg	874
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	
			260					265					270			
ta	ca	ct	ct	gc	ac	cg	ct	tg	ca	ga	at	ga	ga	tg	ga	922
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	
		275					280					285				
tt	gg	gc	ca	ca	tg	tc	ga	gc	ca	ac	tg	gt	aa	tt	ca	970
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	
	290					295					300					
gg	gg	ta	cg	tg	gt	ga	ac	aa	cg	tg	gt	ga	cc	ta	at	1018
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	
305					310					315					320	
ca	gt	tt	ga	aa	cg	tg	ct	tg	cc	gc	tc	aa	cc	ct	tg	1066
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	
				325					330					335		
cg	ga	ca	cc	tc	tc	at	gt	ca	cg	ta	at	ac	at	ac	tc	1114
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	
			340					345					350			
ga	cg	ag	gt	cc	gc	ga	gt	tt	ca	at	ca	gc	ac	tc	gt	1162
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	
		355					360					365				
ta	cc	gg	gc	ta	aa	gc	tt	ca	at	cg	gc	ga	aa	tc	ca	1210
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	
	370					375					380					
gg	ga	tt	ta	at	ag	ca	at	aa	aa	gt	ag	gc	at	ct	gt	1258
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	
385					390					395					400	
ct	gc	cg	cc	gt	ac	gg	cc	cg	ga	ta	gt	ct	ga	ct	ga	1306
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	
				405					410					415		
at	gt	ac	at	aa	tc	ct	at	ag	ta	cg	gc	ag	tc	gt	ct	1354
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	
			420					425					430			
ag	ct	ac	gt	tt	gt	gg	gc	ta	ac	tt	tg	ag	gc	ag	cc	1407
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe						
		435				440										
cc	tc	cc	tc	gc	ag	tc	ac	cc	ta	gc	tc	gt	ag	gc	cc	1467
taa	agg	gaga	aag													1480

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240



Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
 245 250 255  
 Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
 260 265 270  
 Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
 275 280 285  
 Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
 290 295 300  
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
 305 310 315 320  
 Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
 325 330 335  
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
 340 345 350  
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
 355 360 365  
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
 370 375 380  
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Phe Ala Met Leu Val  
 385 390 395 400  
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
 405 410 415  
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430  
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
 435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23  
gctgtggcag aaacccctga cttctgcccc ecacctccca gcctcaggat gctccctttt 60  
gcctcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca 120  
gcgtccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag 180  
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct 240  
tgcaagggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgctct 300  
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa 360  
caaccaaacc cttgcccga gggctacgag cctgatgaac aggagagctg tgtggatgtg 420  
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttcct 480  
ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggaccga atgtgtggac 540  
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt 600  
cgatgccagt gtgagccagg cttccagttg ggacctaa accgctcttg tgtggatgtg 660  
aatgagtgtg acatgggagc cccatgtgag cagcgtgct tcaactccta tgggaccttc 720  
ctgtgtcgt gtaaccagg ctatgagctg caccgggat gcttctctg cagcgatctc 780  
gatgagtgcg gctactccag ttacctctgc cagtacc 817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcaac ggatttggtc gtat 24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atggtggtga agac 24

<210> 26  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> antisense-beta-actin oligonucleotide

<400> 26  
cggttggcct tggggttcag ggggg 25

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sense-MBP1 oligonucleotide

<400> 27  
gccctgatgg ttaccgcaag a 21

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> antisense MBP1 oligonucleotide

<400> 28  
agcccccatg gaagttgaca c 21

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sense-beta-actin oligonucleotide

<400> 29

gtggggcgcc ccaggcacca

20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 30

tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48  
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca 192  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc 240  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att 288  
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac 336  
Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt tac cag ctg ctg 384  
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

gcc aca cgc ctc tgc caa gac att gat gag tgt gag tct ggt gcg cac 432  
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
130 135 140

cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat ggg ggc tac cgc 480  
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc cag gtc tct gag 528  
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
165 170 175

aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt cga gag cag cct 576

Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro		
			180					185					190				
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg	624	
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val		
		195					200					205					
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggg	gcc	672	
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala		
	210					215					220						
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac	720	
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr		
	225				230					235					240		
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	ccg	768	
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro		
				245					250					255			
gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc	atg	816	
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met		
			260					265					270				
aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	agg	ctc	acc	gtc	864	
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val		
		275					280					285					
ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca	ccctccctgc							915	
Phe	Val	Gly	Ala	Tyr	Thr	Phe											
	290					295											
agctacccta	gctgaggagc	ctgttggtgag	gggcagaatg	agaaaggcaa	taaagggaga											975	
aagaaagtcc	tggtggctga	ggtgggagg	tcacactgca	ggaagcctca	ggctggggca											1035	
gggtggcact	tgggggggca	ggccaagtcc	acctaaatgg	gggtctctat	atgttcaggc											1095	
ccagggggccc	ccattgacag	gagctgggag	ctctgcacca	cgagcttcag	tcaccccgag											1155	
aggagaggag	gtaacgagga	gggcggactc	caggccccgg	cccagagatt	tggacttggc											1215	
tggcttgtag	gggtcctaag	aaactccact	ctggacagcg	ccaggaggcc	ctgggttcca											1275	
ttcctaactc	tgcctcaaac	tgtacatttg	gataagccct	agtagttccc	tgggcctgtt											1335	
tttctataaa	acgaggcaac	tgg														1358	

<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro	Glu	Cys	Val	Asp
1				5					10					15	

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

Phe Val Gly Ala Tyr Thr Phe  
 290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>

<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat 48  
 Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
 1 5 10 15

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96  
 Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
 20 25 30

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144  
 Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac 192  
 Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
 50 55 60

aca tgt gag aac aca ccg ggc tcc tac cgc tgc tcc tgc gct gct ggc 240  
 Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
 65 70 75 80

ttc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtg aac gag tgc 288  
 Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
 85 90 95

gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat 336  
 Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
 100 105 110

cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc 384  
 Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
 115 120 125

tgc aca gac atc gat gag tgt gca cag ggc gcg ggc att ctc tgt acc 432  
 Cys Thr Asp Ile Asp Glu Cys Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
 130 135 140

ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag 480  
 Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
 145 150 155 160  
 caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat 528  
 Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
 165 170 175  
 gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac 576  
 Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
 180 185 190  
 aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac 624  
 Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
 195 200 205  
 tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat 672  
 Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
 210 215 220  
 atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc 720  
 Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
 225 230 235 240  
 aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc 768  
 Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
 245 250 255  
 cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag 816  
 Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
 260 265 270  
 ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act 864  
 Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
 275 280 285  
 ggt gtg gta tcc ctg cag cgg tct gtt ctg gag ccg cgg gac ttt gcc 912  
 Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
 290 295 300  
 cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320  
 ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca 1009  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330  
 tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tcctaagtgg 1069  
 ctttttgctg tgactctgta acttaactta atcatgctga gctggttggt cttgagtctc 1129  
 taccctagag ggagggagat gcaccccagc aggcactgag tacaggccag ggtcaccgca 1189  
 ggctagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc 1249  
 aactatggct acagctgaca ttccattcct tcatccactg tgttcctcaa ttaaaaaaaa 1309  
 aaatcagctg tgcattgtag cacagacctt taatcctagc actggggagg cagaggtagg 1369  
 tagatctctg agttccaggc cagcctgggtc tacactggga gttctaacca gccagagcta 1429  
 catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc 1489



agcctggtct acgctgggag ttctaaccag ccagagctac atagagagat cctatctcaa 1549  
 caaggaaaaa tgaaagaaat ctttttaaaa ggtttttttt tttgctgttg ttgtttaatg 1609  
 ataagagtag cacatataca ttatttaaaaa tgatcaaata gcacagaaag gtta 1663

<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
 1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
 65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
 85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
 100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
 115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
 130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
 145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
 165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
325 330